What is claimed is:

1.   A method of diagnosing liver cancer in a patient, comprising:

(a) detecting the level of expression in a tissue sample of two or more genes from Tables 3-9; wherein differential expression of the genes in Tables 3-9 is indicative of

5   liver cancer.

2.   A method of detecting the progression of liver cancer in a patient, comprising:

(a) detecting the level of expression in a tissue sample of two or more genes

10   from Tables 3-9; wherein differential expression of the genes in Tables 3-9 is indicative of liver cancer progression.

3.   A method of monitoring the treatment of a patient with liver cancer, comprising:

15   (a)   administering a pharmaceutical composition to the patient;

(b)   preparing a gene expression profile from a cell or tissue sample from the patient; and

(c)   comparing the patient gene expression profile to a gene expression from a cell population selected from the group consisting of normal liver cells,

20   hepatocellular carcinoma and metastatic liver carcinoma.

4.   A method of treating a patient with liver cancer, comprising:

(a)   administering to the patient a pharmaceutical composition, wherein the composition alters the expression of at least one gene in Tables 3-9;

25   (b)   preparing a gene expression profile from a cell or tissue sample from the patient comprising tumor cells; and

(c)   comparing the patient expression profile to a gene expression profile selected from the group consisting of normal liver cells, hepatocellular carcinoma and metastatic liver carcinoma

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5.   A method of diagnosing hepatocellular carcinoma in a patient, comprising:

(a) detecting the level of expression in a tissue sample of two or more genes from Tables 3-9; wherein differential expression of the genes in Tables 3-9 is indicative of hepatocellular carcinoma.

5   6.   A method of detecting the progression of hepatocellular carcinoma in a patient, comprising:

(a) detecting the level of expression in a tissue sample of two or more genes from Tables 3-9; wherein differential expression of the genes in Tables 3-9 is indicative of hepatocellular carcinoma progression.

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7.   A method of monitoring the treatment of a patient with hepatocellular carcinoma, comprising:

(a)   administering a pharmaceutical composition to the patient;

(b)   preparing a gene expression profile from a cell or tissue sample from
15   the patient; and

(c)   comparing the patient gene expression profile to a gene expression from a cell population comprising normal liver cells or to a gene expression profile from a cell population comprising hepatocellular carcinoma cells or to both.

20   8.   A method of treating a patient with hepatocellular carcinoma, comprising:

(a)   administering to the patient a pharmaceutical composition, wherein the composition alters the expression of at least one gene in Tables 3-9;

(b)   preparing a gene expression profile from a cell or tissue sample from the patient comprising hepatocellular carcinoma cells; and

25   (c)   comparing the patient expression profile to a gene expression profile from an untreated cell population comprising hepatocellular cells.

9.   A method of diagnosing a metastatic liver tumor in a patient, comprising:

(a) detecting the level of expression in a tissue sample of two or more genes from Tables 3-9; wherein differential expression of the genes in Tables 3-9 is indicative of metastatic liver cancer.

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10.   A method of detecting the progression of a metastatic liver cancer in a patient, comprising:

(a) detecting the level of expression in a tissue sample of two or more genes from Tables 3-9; wherein differential expression of the genes in Tables 3-9 is indicative of a metastatic liver cancer progression.

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11   A method of monitoring the treatment of a patient with a metastatic liver cancer, comprising:

(a)   administering a pharmaceutical composition to the patient;

(b)   preparing a gene expression profile from a cell or tissue sample from the patient; and

(c)   comparing the patient gene expression profile to a gene expression from a cell population comprising normal liver cells or to a gene expression profile from a cell population comprising metastatic liver tumor cells or to both.

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12.   A method of treating a patient with a metastatic liver tumor, comprising:

(a)   administering to the patient a pharmaceutical composition, wherein the composition alters the expression of at least one gene in Tables 3-9;

(b)   preparing a gene expression profile from a cell or tissue sample from the patient comprising metastatic liver tumor cells; and

(c)   comparing the patient expression profile to a gene expression profile from an untreated cell population comprising metastatic liver tumor cells.

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13.   A method of differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, comprising::

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(a) detecting the level of expression in a tissue sample of two or more genes from Tables 3-9; wherein differential expression of the genes in Tables 3-9 is indicative of metastatic liver cancer rather than hepatocellular carcinoma.

14.   A method of screening for an agent capable of modulating the onset or progression of liver cancer, comprising:

(a)   preparing a first gene expression profile of a cell population comprising liver cancer cells, wherein the expression profile determines the expression level of one or more genes from Tables 3-9 ;

(b)   exposing the cell population to the agent;

(c)   preparing second gene expression profile of the agent-exposed cell population; and

(d)   comparing the first and second gene expression profiles.

15.   The method of claim 14, wherein the liver cancer is a hepatocellular carcinoma.

16.   The method of claim 14, wherein the liver cancer is a metastatic liver cancer.

17.   A composition comprising at least two oligonucleotides, wherein each of the oligonucleotides comprises a sequence that specifically hybridizes to a gene in Tables 3-9 .

18.   A composition according to claim 17, wherein the composition comprises at least 3 oligonucleotides.

19.   A composition according to claim 17, wherein the composition comprises at least 5 oligonucleotides.

20.   A composition according to claim 17, wherein the composition comprises at least 7 oligonucleotides.

21.   A composition according to claim 17, wherein the composition comprises at least 10 oligonucleotides.

22.   A composition according to any one of claims 17-21, wherein the oligonucleotides are attached to a solid support.

23.   A composition according to claim 22, wherein the solid support is selected from a group consisting of a membrane, a glass support, a filter, a tissue culture dish, a polymeric material, a bead and a silica support.

24.   A solid support comprising at least two oligonucleotides, wherein each of the oligonucleotides comprises a sequence that specifically hybridizes to a gene in Tables 3-9.

25.   A solid support according to claim 24, wherein the oligonucleotides are covalently attached to the solid support.

26.   A solid support according to claim 24, wherein the oligonucleotides are non-covalently attached to the solid support.

27.   A solid support according to claim 24, wherein the support comprises at least about 10 different oligonucleotides in discrete locations per square centimeter.

28.   A solid support according to claim 24, wherein the support comprises at least about 100 different oligonucleotides in discrete locations per square centimeter.

29.   A solid support according to claim 24, wherein the support comprises at least about 1000 different oligonucleotides in discrete locations per square centimeter.

30.   A solid support according to claim 24, wherein the support comprises at least about 10,000 different oligonucleotides in discrete locations per square centimeter.

31.   A computer system comprising:

(a) a database containing information identifying the expression level in liver tissue of a set of genes comprising at least two genes in Tables 3-9 ; and

(b) a user interface to view the information.

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32.   A computer system of claim 31, wherein the database further comprises sequence information for the genes.

33.   A computer system of claim 31, wherein the database further comprises
10   information identifying the expression level for the set of genes in normal liver tissue.

34.   A computer system of claim 31, wherein the database further comprises information identifying the expression level of the set of genes in liver cancer tissue.

15   35.   A computer system of claim 34, wherein the liver cancer tissue comprises hepatocellular carcinoma cells.

36.   A computer system of claim 34, wherein the liver cancer tissue comprises metastatic liver cancer cells.

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37.   A computer system of any of claims 31-36, further comprising records including descriptive information from an external database, which information correlates said genes to records in the external database.

25   38.   A computer system of claim 37, wherein the external database is GenBank.

39.   A method of using a computer system of any one of claims 31-36 to present information identifying the expression level in a tissue or cell of at least one gene in Tables 3-9, comprising:

30   (a) comparing the expression level of at least one gene in Tables 3, 4, 5, 6, 8 or 3-9 in the tissue or cell to the level of expression of the gene in the database.

40.   A method of claim 39, wherein the expression level of at least two genes are compared.

41.   A method of claim 39, wherein the expression level of at least five genes are compared.

42.   A method of claim 39, wherein the expression level of at least ten genes are compared.

43.   A method of claim 39, further comprising displaying the level of expression of at least one gene in the tissue or cell sample compared to the expression level in liver cancer.

44.   A kit comprising at least one solid support of any one of claims 24-30 packaged with gene expression information for said genes.

45.   A kit of claim 44, wherein the gene expression information comprises gene expression levels in a tissue or cell sample exposed to a nephrotoxin.

46.   A kit of claim 45, wherein the gene expression information is in an electronic format.